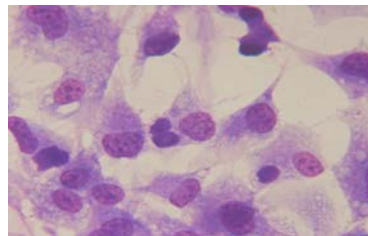


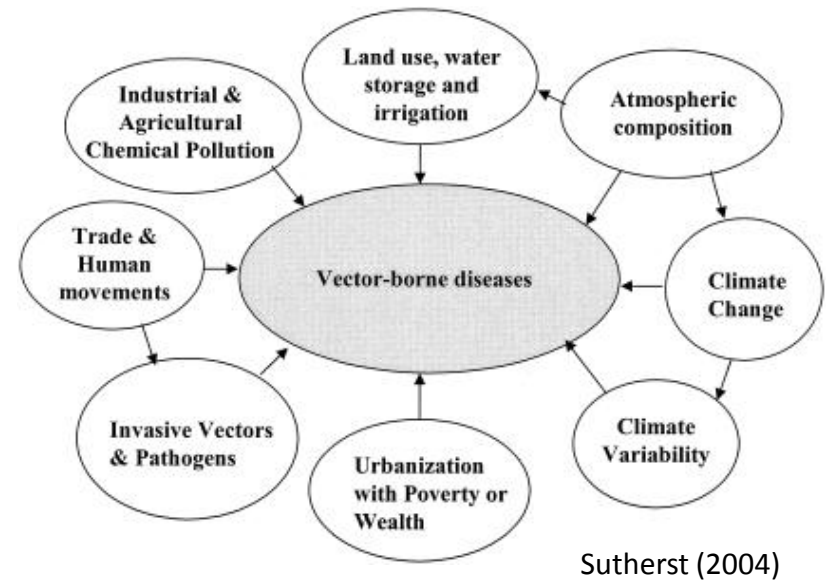
Vector-pathogen association: lack of congruence of
phylogeographical pattern of the vector tick
Amblyomma variegatum (Acari: Ixodidae) and of the
Rickettsiales *Ehrlichia ruminantium*?

K. Huber, N Vachieri, H. Adakal, N Cangi, J
Gordon, N Haddad, L das Neves and F.
Stachurski



Human activities

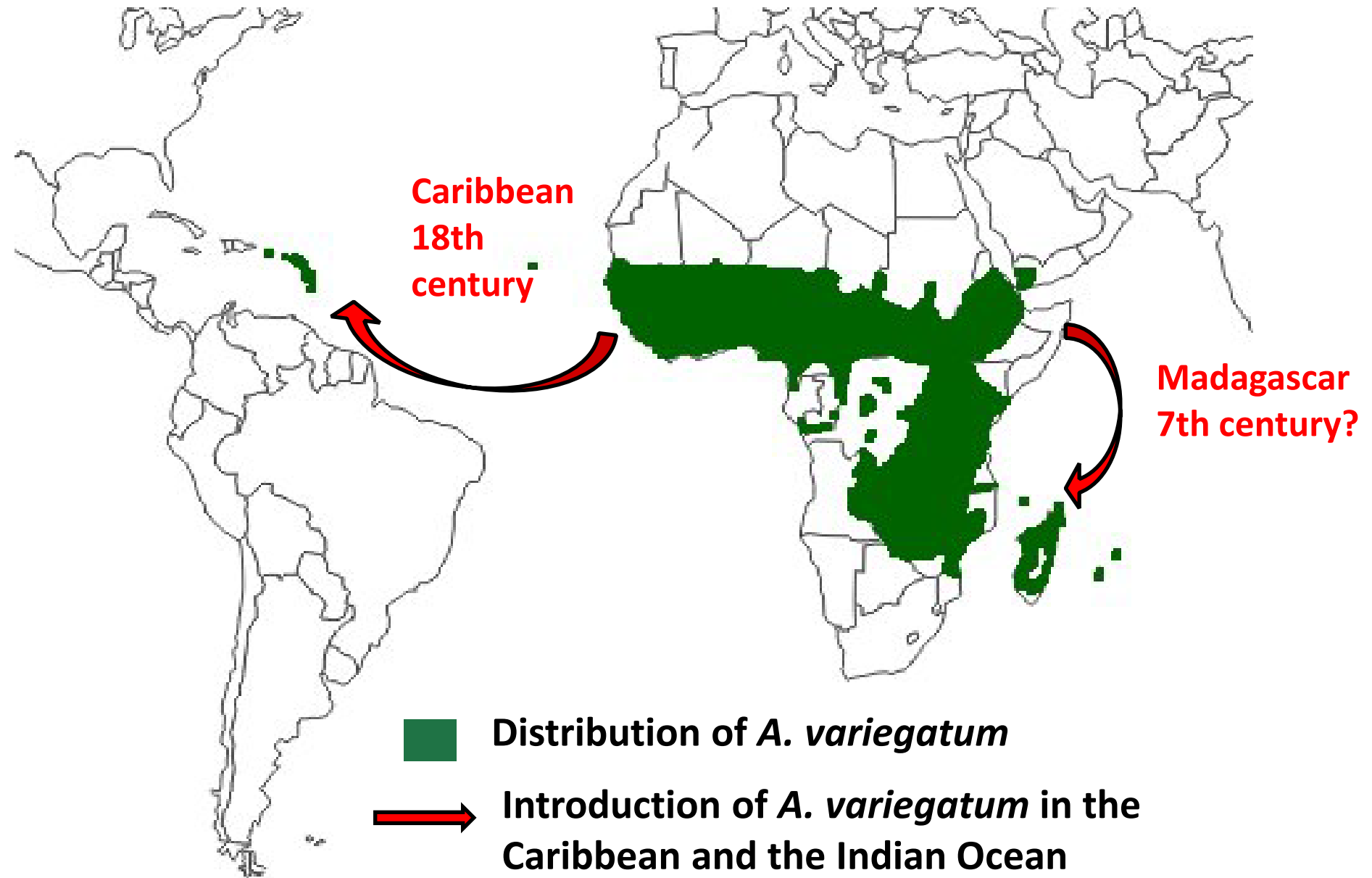
- Alteration of natural ecosystems: affect the transmission cycles of vector-borne infectious diseases
- Change in migration regime (human activities)
- Environmental change increasing the number of suitable habitats: global warming, human impact on landscape

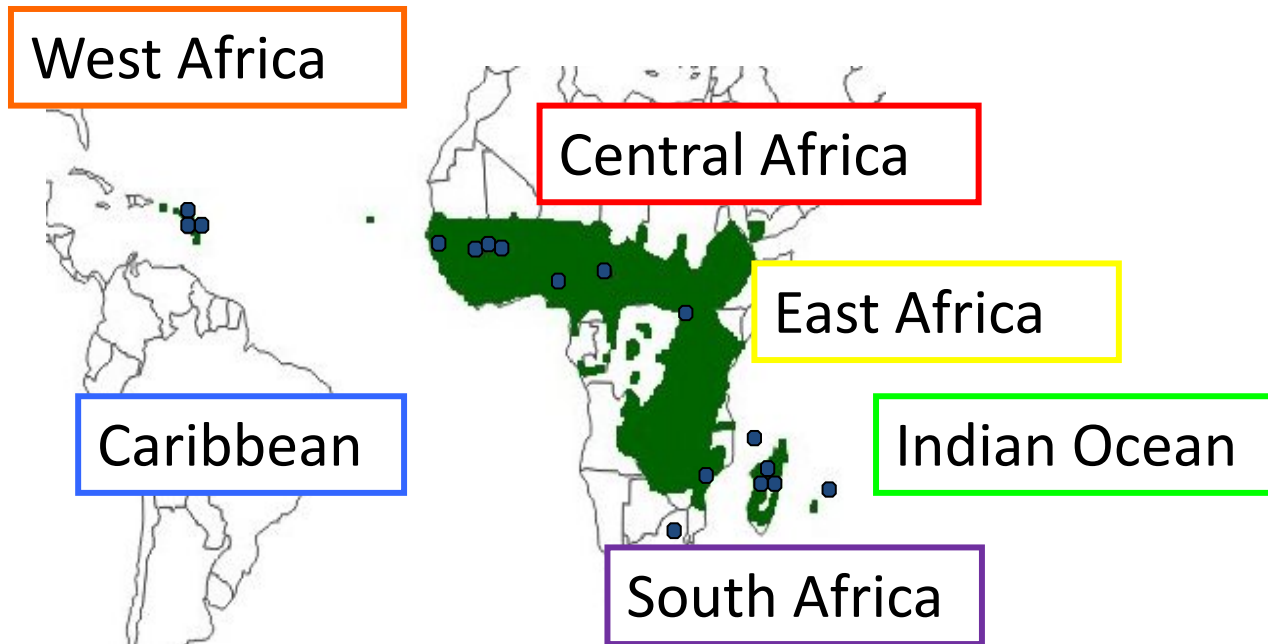


Amblyomma variegatum and *Ehrlichia ruminantium*

- *Amblyomma variegatum*: hard tick of the family Ixodidae which infests livestock and wildlife
- Causes substantial economic losses by blood predation (low live weight gains, reduced milk yield) and physical injury (wound)
- Main vector of *Ehrlichia ruminantium* the pathogen responsible for heartwater or cowdriosis, a tropical disease of ruminants







- Distribution of *A. variegatum*
- Collection sites

Amblyomma variegatum

408 pb of the mtDNA 16s

433 pb of the mtDNA cytochrome b



Ehrlichia ruminantium

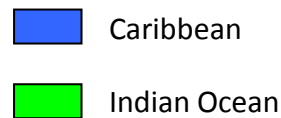
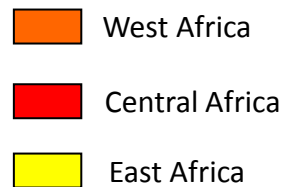
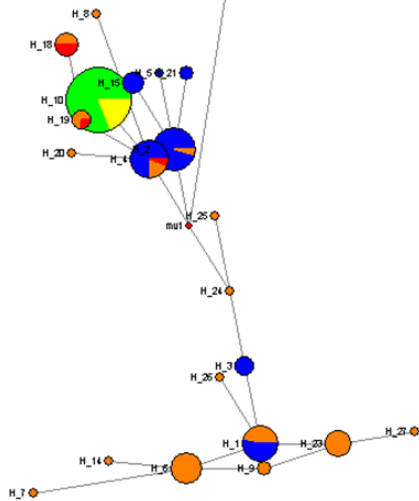
Multi-Locus Sequence Typing (5 housekeeping genes)

Amblyomma variegatum

Cytb

East Africa
+
Indian Ocean

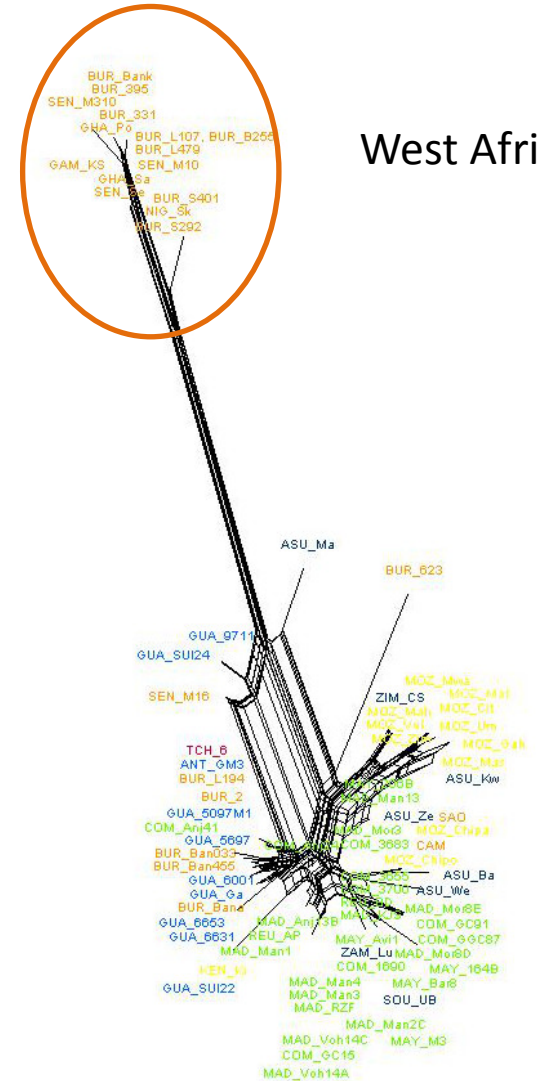
16S



Median joining networks

Ehrlichia ruminantium

West Africa



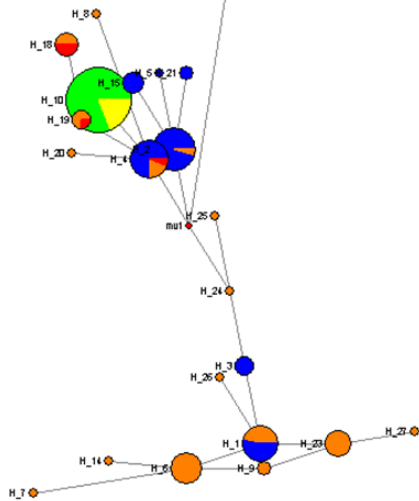
Split decomposition neighbor-net

Amblyomma variegatum

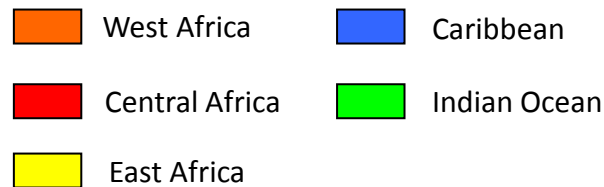
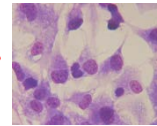
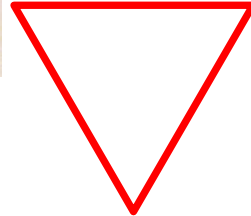
Cytb

East Africa
+
Indian Ocean

16S

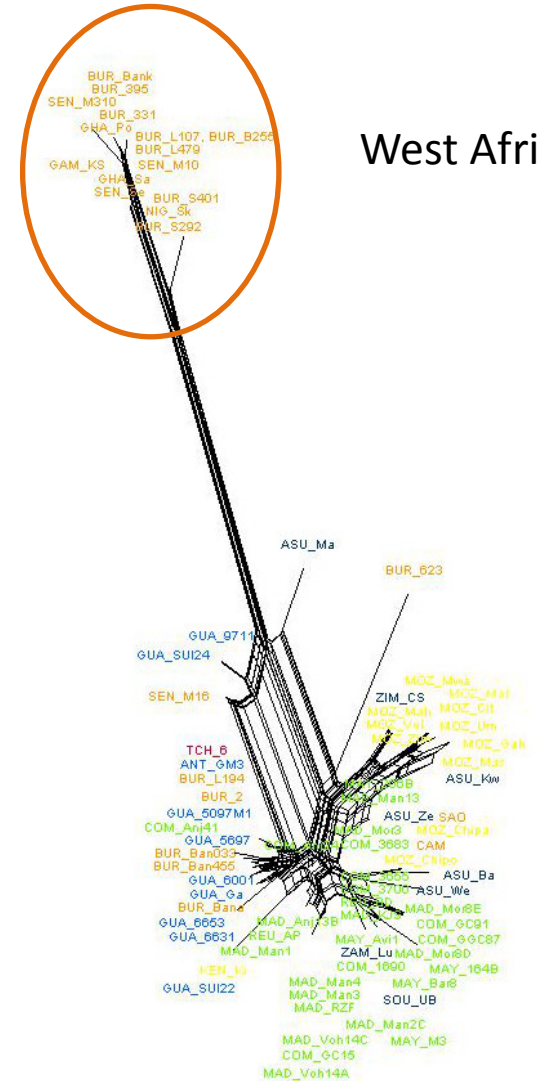


Median joining networks



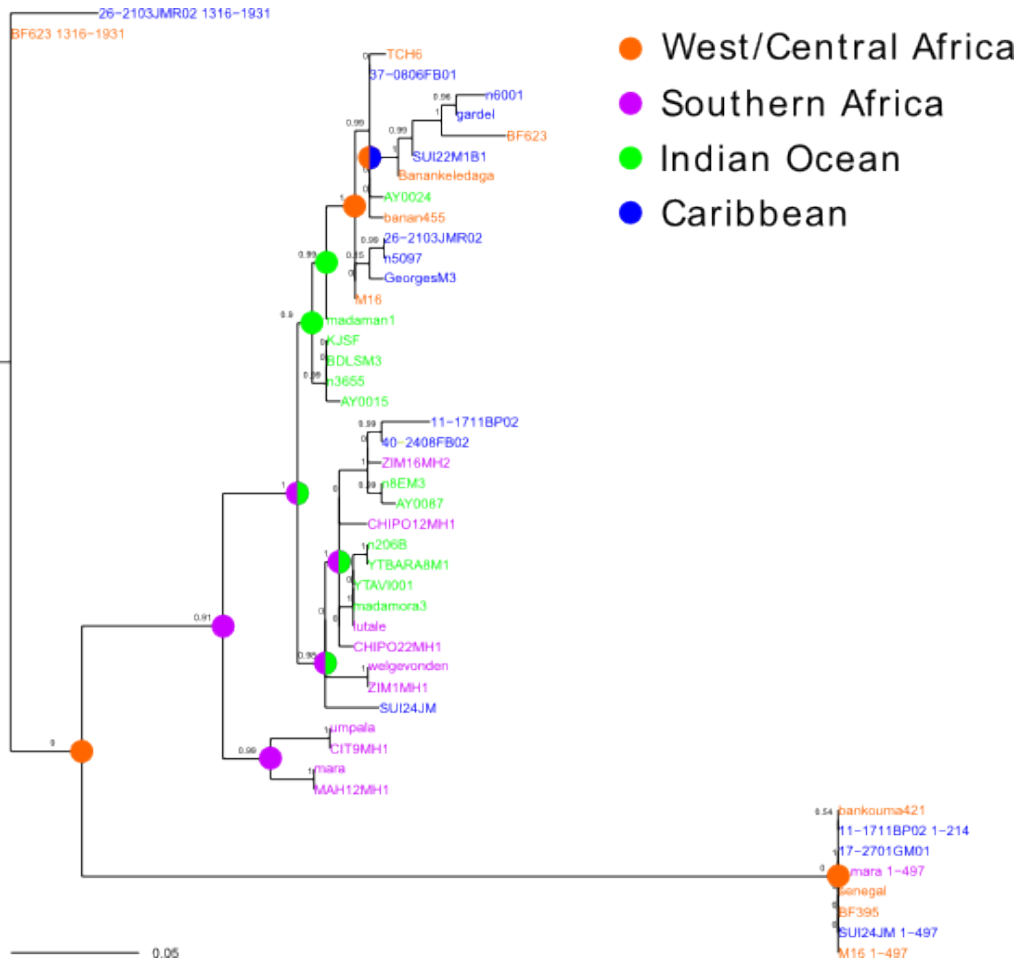
Ehrlichia ruminantium

West Africa

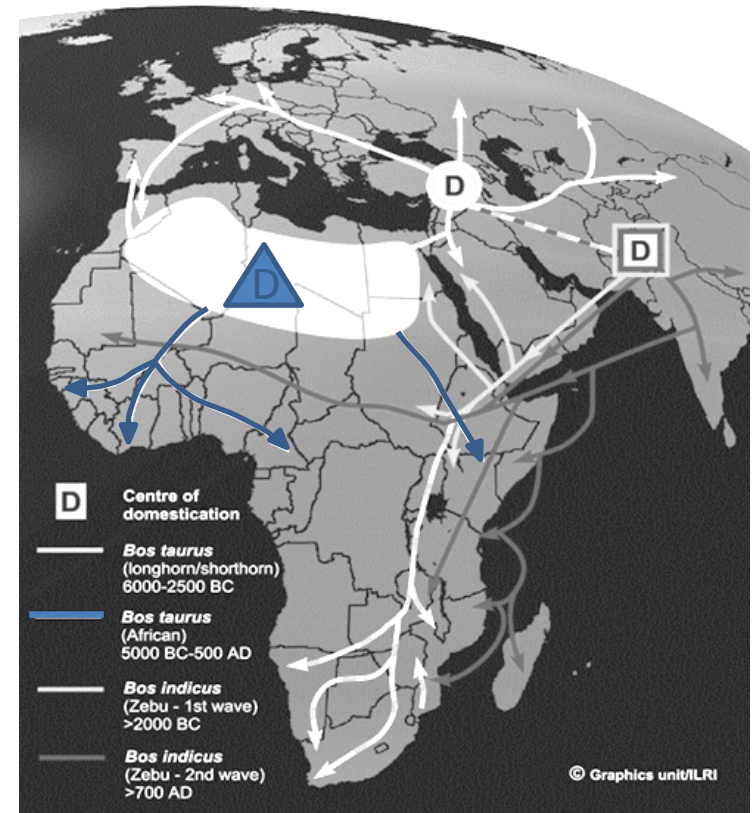


Split decomposition neighbor-net

MLST
ML
TPM1uf+I



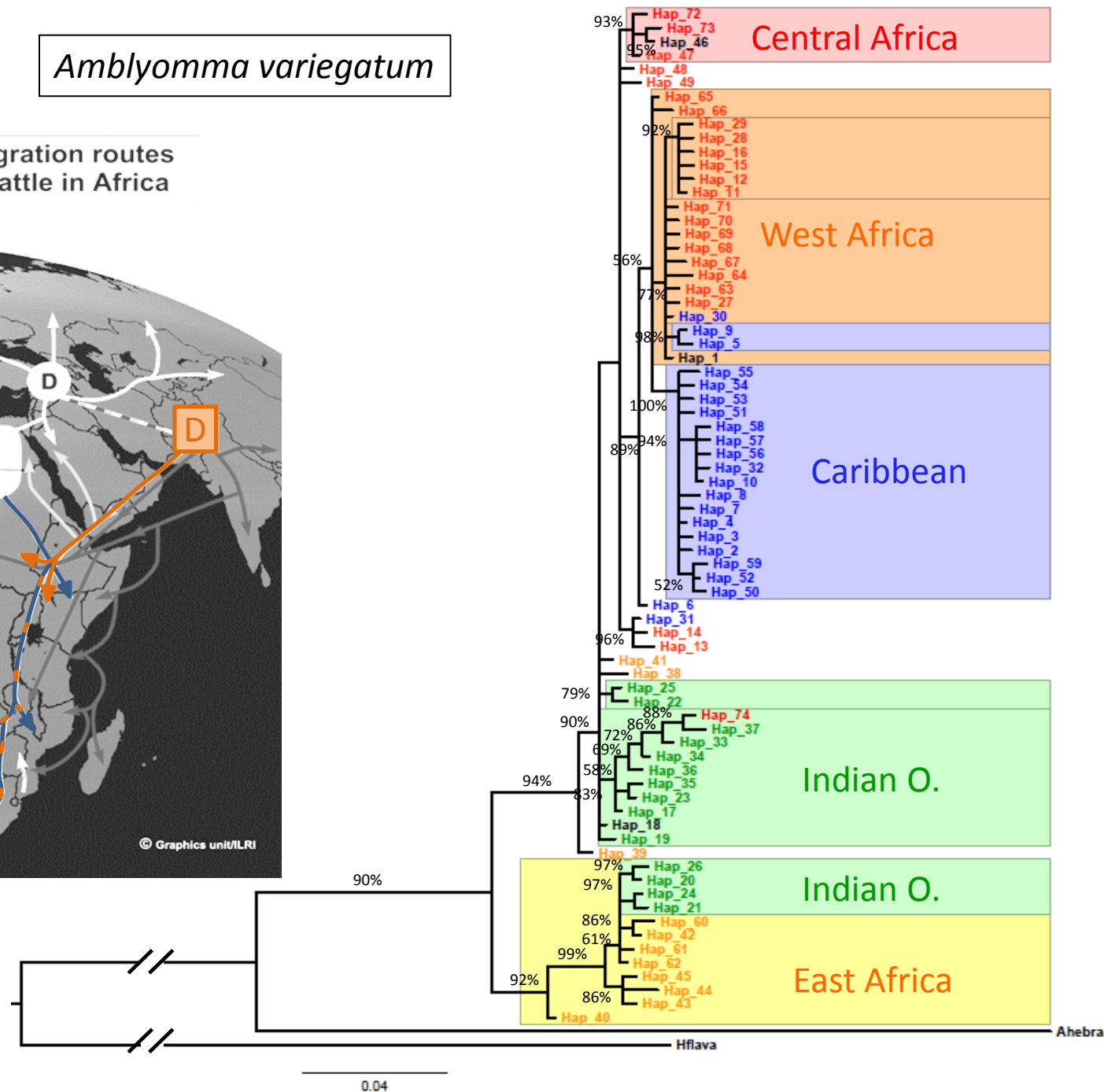
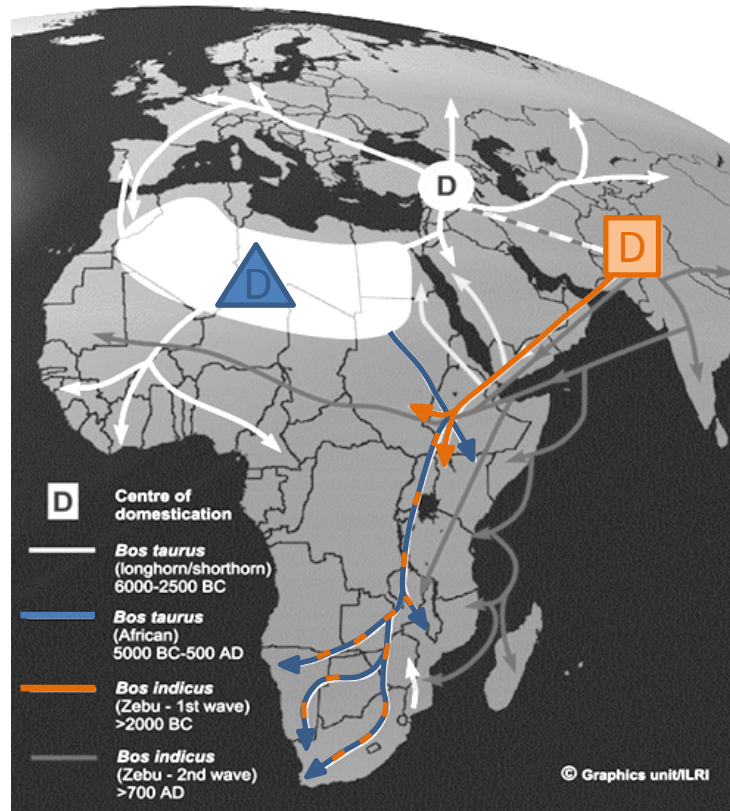
Origin and migration routes of domestic cattle in Africa



Ehrlichia ruminantium

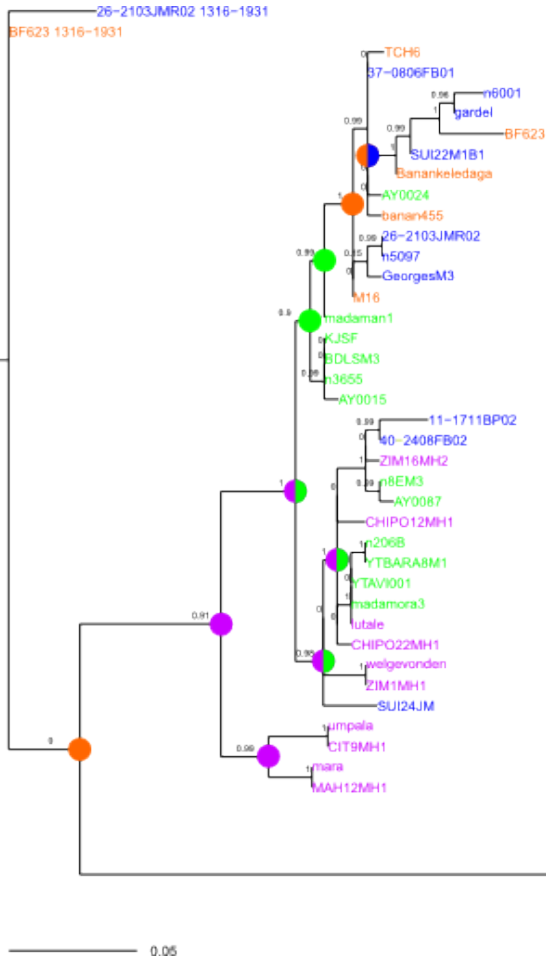
HKY+GTR

Origin and migration routes of domestic cattle in Africa



MLST
ML
TPM1uf+l

16S Fst = 0.29647
P = **0.00098**
Cytb Fst = 0.36853
P = **0.01466**



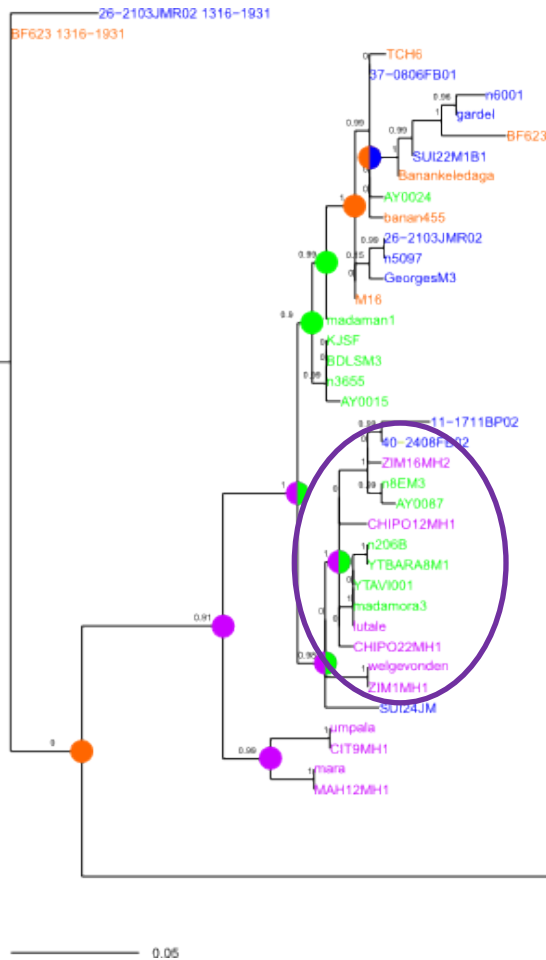
- West/Central Africa
- Southern Africa
- Indian Ocean
- Caribbean



Ehrlichia ruminantium

Amblyomma variegatum

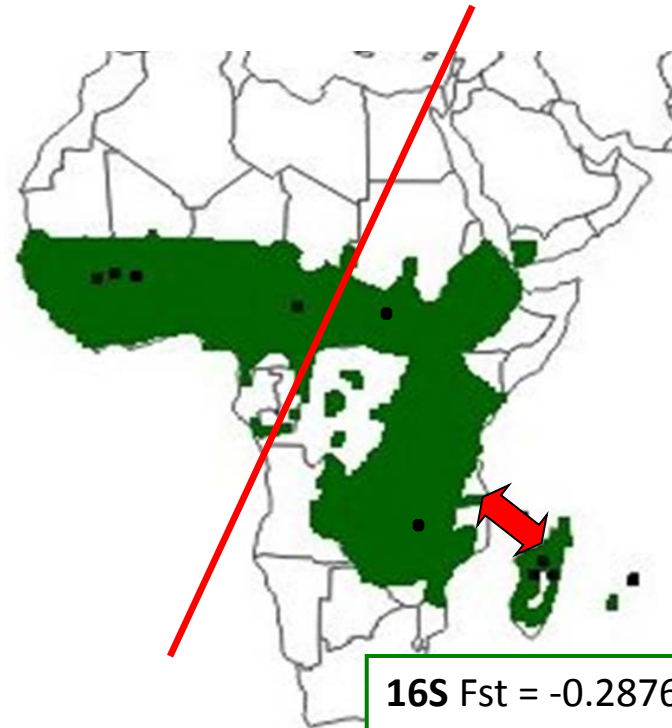
MLST
ML
TPM1uf+l



Ehrlichia ruminantium

- West/Central Africa
- Southern Africa
- Indian Ocean
- Caribbean

16S Fst = 0.29647
P = **0.00098**
Cytb Fst = 0.36853
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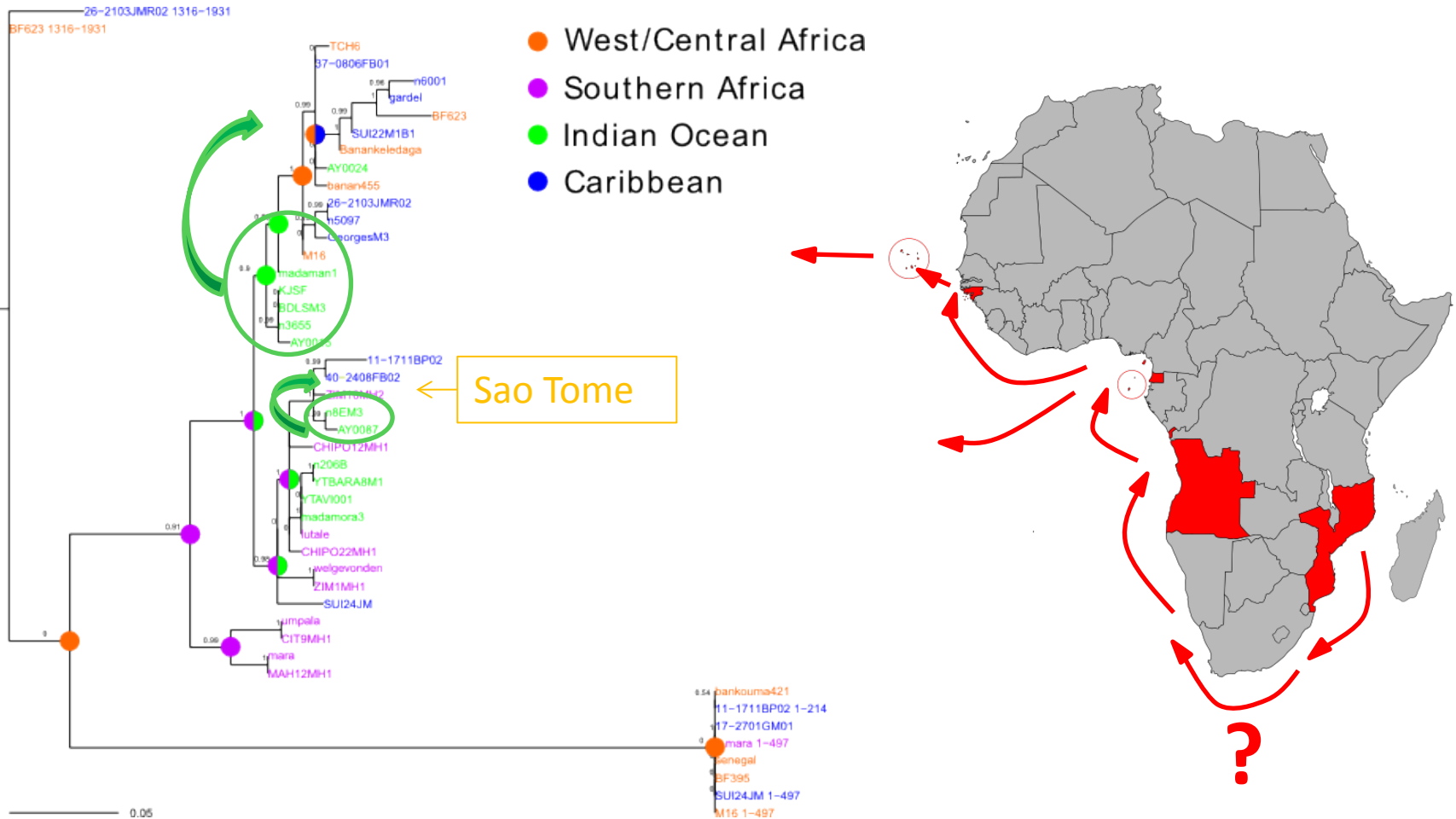
16S Fst = -0.28769
P = 0.90909
Cytb Fst = -0.23937
P = 0.69404

Amblyomma variegatum

TPM1uf+I



TPM1uf+I



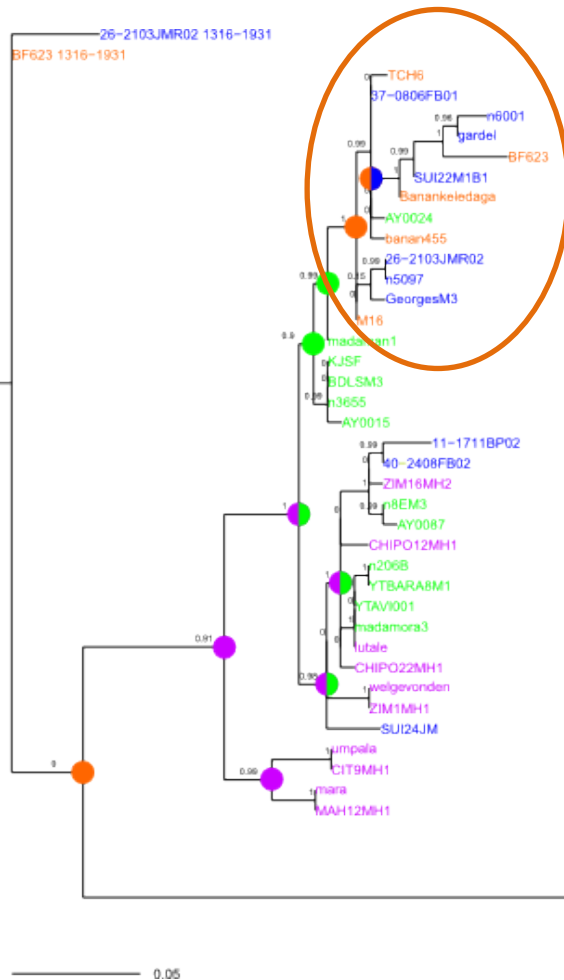
Ehrlichia ruminantium

Hypothesis : Portuguese colonies and trade posts

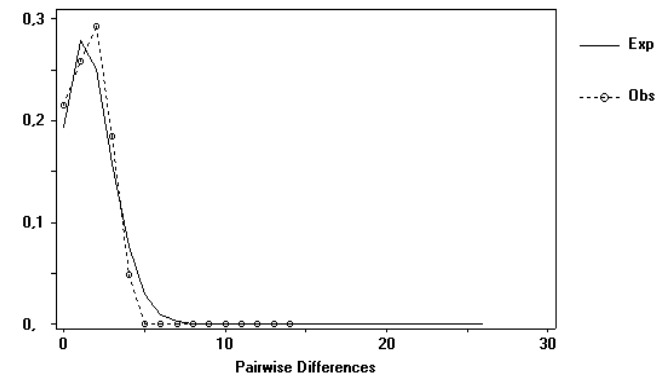
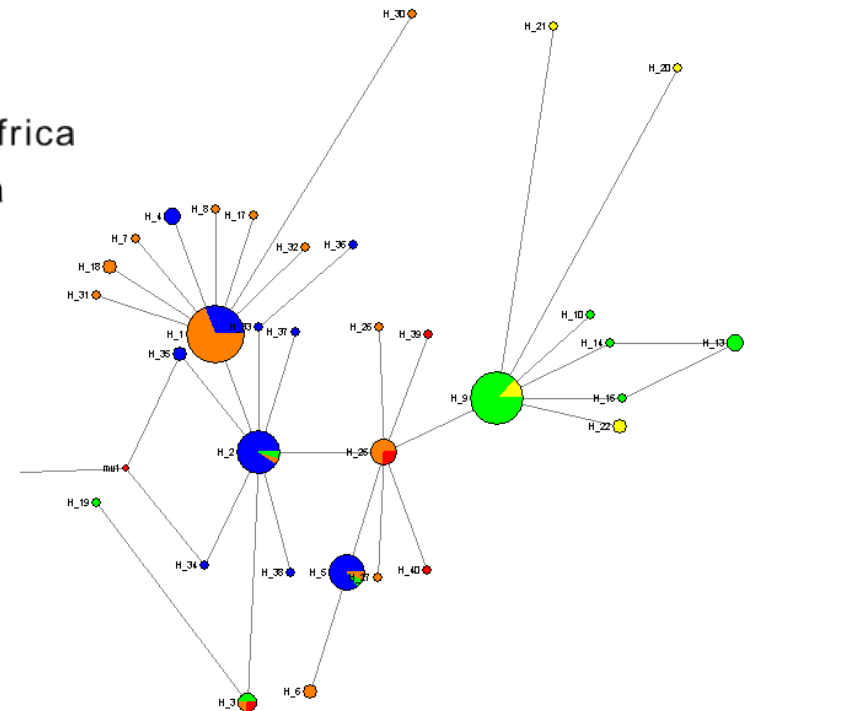
MLST
ML
TPM1uf+I

Median joining networks (Cytb)

- West/Central Africa
- Southern Africa
- Indian Ocean
- Caribbean



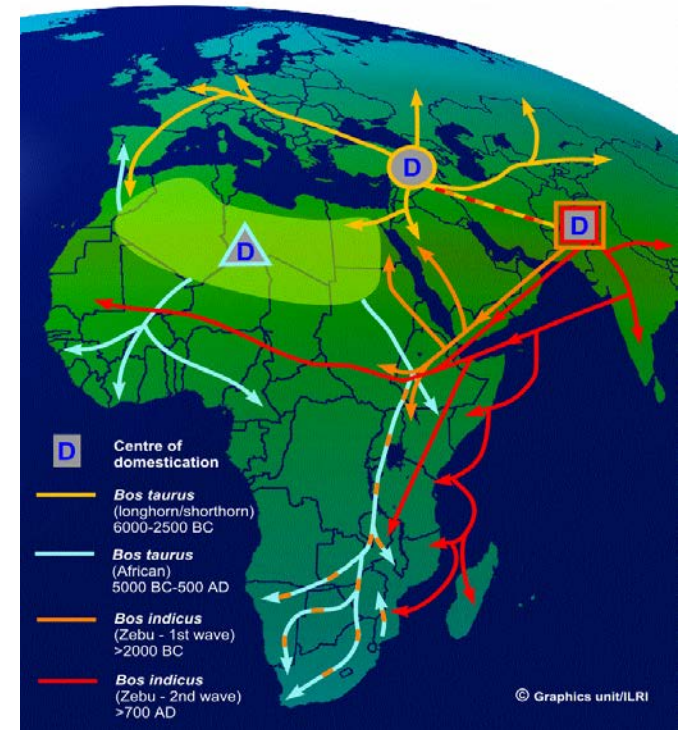
Ehrlichia ruminantium



Amblyomma variegatum

Conclusion

- Apparent lack of congruence between *A. variegatum* and *E. ruminantium*
- But a common history in relation to cattle movements
- Complex interactions between host, pathogen and vector : multiple evolutionary steps for mutual adaptation



Acknowledgments

This work was granted by :

GIS-CRVOI (projet DIGEERAV-OI)

INRA AIP Bio-Ressources 2008 et CIRAD-INRA

Fundings EU projects

FEDER project « Gestion des risques en santé animale et végétale »

EPIGENESIS project "European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement No 31598

We also thank R. Pegram, M. Frebling, M. Asnaoui, M. Saimo, A. Boulanger, and M.R. Jaumally for tick samples collection

